Valorisation of cotton germplasm collections, securing and developing exchanges in compliance with international agreements

74th ICAC Plenary Meeting, 6-11 December 2015, Mumbai, India.
https://www.icac.org/getattachment/mtgs/Plenary/74th-Meeting/Agenda/OS8_Bachelier.pdf

Christopher VIOT[1], Najate MAGHNAOUI[1], Claire NEIRAC[2], Dominique DESSAUW[3] & Bruno BACHELIER[4]
CIRAD [1]Bios - UMR AGAP, [2]Dgdrd, [3]Bios - UMR PVBMT, [4]Persyst – UPR AIDA
Contact: christopher.viot@cirad.fr

Abstract
International treaties and national legislations organize and secure genetic resources exchanges, but, at the same time, they make them more and more complex and restrictive. Meanwhile, the exploration and exploitation of plant germplasm resources have become easier and cheaper with present-day high-throughput, low-cost genotyping technologies, efficient phenotyping systems, and powerful tools for bioinformatics and statistical analyses. Cotton genetic resources are more and more needed for continued progress in yield, fibre quality, pest resistance, adaptation to climate change and marginal environments. Many traits of high breeding value are present in the cotton germplasm resources, some being already exploited, some under intensive research efforts, and probably many others we can expect to be present. In the new regulatory context limiting or impeding germplasm exchanges, solutions for pursuing and developing the study, the valorisation and the protection of cotton germplasm collections can benefit from the new scientific tools and international cooperation.

Regulatory context for transfers of cotton (G*ossypium* sp.) genetic resources
At the beginnings, there was nothing. The main global framework for germplasm exchanges was the phytosanitary regulations. More than 50 years ago, the UPOV was created to protect new varieties of plants; modified versions appeared at different dates. Thus, the UPOV regulates protected varieties, which is a part of the useful genetic resources. More recently was created the CBD, the Convention on Biological Diversity, in 1992. The CBD has put genetic resources under the jurisdiction and sovereignty of national governments. It thus brought regulation to the access to genetic resources, but also of traditional knowledge associated with the genetic resources. Philosophy is:
- Regulation by states, above property rights
- Link to origin of the genetic resources.
The CBD is a multilateral treaty now signed by 195 states and the European Union; it entered into force at the end of 1993.

Supplementary international agreements: Cartagena protocol
The CBD was complemented by two new agreements. The first one, in 2000, was the Cartagena Protocol on Biosafety, or « Biosafety Protocol ». The Cartagena protocol is intended to protect the natural biological diversity from risks by living modified organisms from modern biotechnology. It is important for geographic areas where there still exist natural populations of wild cotton plants.

Nagoya protocol
The second supplementary protocol was the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization. The Nagoya Protocol aims at clarifying the article 15 of the CBD about Fair Sharing of Benefits, in order to create greater legal certainty and transparency for both providers and users of genetic resources. It is to be remembered

that the traditional knowledge associated to genetic resources is to be considered on the same level as the genetic resource itself.

Material Transfer Agreements

Another very important international treaty was adopted meanwhile, in 2001, the International Treaty on Plant Genetic Resources for Food and Agriculture. It was promoted by the FAO. This treaty is aiming at an open access to genetic resources useful to agriculture and breeding. This treaty deals only with agricultural genetic resources essential for food security. Thus cotton is not among the crops listed, but the treaty helps emphasizing the importance of access to genetic resources, and thus international exchanges, for present and future agriculture. The whole system is not at all simple! But for cotton, the main regulatory context for exchanges of cotton germplasm is comprised of the initial CBD, the Nagoya protocol and the UPOV agreements dealing with protected varieties. Most important are:

- The necessity for agreements between parties exchanging genetic resources, under the control of national regulations, and
- The obligation for sharing of benefits resulting from the use of these genetic resources, including the associated traditional knowledge. The Nagoya Protocol about fair sharing of benefits appears to specialists as potentially very problematic; Sixty nine countries ratified this protocol and thirty nine have implemented legislative, administrative or policy measures.

Geographic distribution of species from the genus Gossypium

The distribution of Gossypium species world-wide is shown in this map. It is the natural areas of occurrence of the plants for each species. Each species is characterized in the wild by a geographic area where its plants can be encountered. Over this this area, plants of a given species will show some genetic diversity, linked to diverse adaptive characteristics; this genetic diversity brings useful genes for breeding. Four cotton species are cultivated, the two main ones being the American tetraploids, while the 2 Old-World diploids are nowadays grown on limited areas apart from modern agriculture. There are approximately 45 diploid and five tetraploid species. The wild species can cross, more or less easily, with cultivated cottons and are potential sources for useful genes. The Gossypium species is consequently classified in three germplasm pools according to the difficulties of crossing and gene transfer towards the 2 main cultivated tetraploids, G. hirsutum and G. barbadense:

- In blue are the cultivated tetraploid species and the other tetraploids, which cross rather easily.
- In green are the wild diploid species with which gene transfer is not too difficult.
- In red, gene transfer would be very difficult and thus slow and expansive. It includes all Australian species and some species of the Arabian Peninsula and Eastern Africa.

The natural germplasm resources of cotton are thus extensive, dispersed globally across five continents, but are not present in all cotton-producing countries, and all species are not equally useful for breeding. Some germplasm of the diploid species have already been used as sources of useful genes.

Major ex-situ Gossypium germplasm collections and cotton production

The map shows the location of major Gossypium gene banks and the geographic distribution of cotton production. Maybe some smaller cotton producing countries are not shown. Gene banks are *ex situ* collection, that is "off-site" collection; they are outside of the natural habitat of the species. Mainly, they guard seeds of determined genotypes. Two big gene banks are not within cotton-producing countries, those of Russia and France, but they serve much for international exchanges. The present data do not show the smaller cotton germplasm collections, which certainly possess very valuable collections. Moreover, what we know is that cotton-producing countries frequently possess breeding programs, with collections of varieties, old and recent. Farmers, too, keep traditional or obsolete varieties. Thus smaller producing countries maintain collections of germplasm either for breeding programs or other reasons. There is thus a complex status of the cotton germplasm resources.

Complex status of the cotton genetic resources

There is thus a complex status of the cotton genetic resources. Among all these types of germplasms, potential for breeding can be very different. There are:

- The cultivated species, with: natural populations, and ancient, traditional or modern varieties;
- The wild species.

There are:

- *Ex situ* gene banks of all types of germplasms, well characterized
- Small collections, which are much less well known
- Natural populations and traditional varieties or landraces could be the most useful gene reservoirs.

Some of these germplasm resources can be considered at high risk.

Examples of improvement needs and identified gene sources

The slide illustrates that very interesting possibilities are offered by the Gossypium germplasms as sources of useful genes. On the left side are traits with genetic improvement needs, or foreseeable objectives of genetic improvement, for *G. hirsutum* and *G. barbadense*, and on the right side are the donor germplasms. There have been useful donor germplasms identified for many traits, and in particular:

- Resistance to abiotic stress such as drought
- Resistance to biotic stresses: the continually changing spectrum of diseases and pests needs perpetually new genes, and this is accelerated by climate change.

Even fibre quality has found contributors in the wild germplasm. As for yield, up in the slide, it is a complex trait and precise potential gene sources are not easy to identify.

Cotton genetic resources insufficiently exploited

Cotton genetic resources present an enormous potential for varietal improvement, but they are nevertheless insufficiently exploited. The study of the diversity of commercial cotton cultivars and advanced germplasm lines has shown there is a high degree of genetic uniformity within cultivated G. hirsutum, with DNA-based genetic diversity methods. This genetic uniformity impairs adaptation potential and is a vulnerability risk, either to emerging pests, to environmental change, or to competition, as progress potential is limited. How could we enhance the use of cotton genetic resources in varietal improvement?

Different points about cotton germplasm and breeding

Different points may be taken into consideration:

- New genes are needed.
- Most countries do not have sufficient germplasm resources for long term genetic improvement.

Technical possibilities are now extraordinary, but gene search was rendered difficult for diverse other reasons, somewhat paradoxically. Difficulties are:

- Costs (as cotton is not a food staple and thus not a priority in the financially stressed international context)
- High sophistication of these activities
- And complexity of access to germplasm.

Progresses of tools to study the germplasm are in particular:

- In genetics and genomics: high-throughput instruments and dropping costs, available cotton genomes sequences since 2012, for the diploids *G. raimondii* and *G. arboreum*, and for the cultivated tetraploids, with gene annotations
- Mathematical tools for gene search, particularly association genetics (derived from the method to detect genes in human populations)
- In phenotyping: it is frequently the biggest challenge, but new instruments, automated facilities and accumulated knowledge and softwares about plant physiology are facilitating and accelerating plant phenotyping.

Different points about cotton germplasm and breeding

We can further note that there is an asymmetry between owners of germplasm resources and private companies or other institutions able to study and commercially valorise them. This asymmetry is considered a risk by germplasm owners and it certainly hampers germplasm exchanges. Germplasm exchange has become a more sensitive issue as the potential economic impact of germplasm has become more widely recognized. Genome-editing tools change definitely the approach to crop improvement for some traits. There is a need to associate small countries to research projects.

Different points about cotton germplasm and breeding

There is a real need for pursuing prospection efforts in order to ensure that natural populations of cotton plants and traditional varieties or landraces be characterized and collected for gene banks or other ex-situ collections.

It is even sometimes urgency, in order to prevent the loss of important genetic diversity because of habitat loss, modernization of agriculture and disappearance of farmers that use or conserve landraces or dooryard cottons. This urgency of collecting efforts is absolutely new.

It is to be noted that too strict a protection can be very detrimental.

Financial return to collections is of utmost importance, because costs are now high for gene banks and other related activities.

Begin with standardization for plant descriptors and genotyping

Two concrete proposals are to work collectively for:

1- The definition of common plant descriptors to be used in cotton collections, including evaluation of useful traits. This includes adequate protocols. Characterization and evaluation of germplasm is perhaps the greatest challenge facing existing gene banks and other collections. All major collections characterize their collections with phenotypic descriptors. In many instances descriptors are botanical or taxonomic. There is need of agronomic traits of interest to breeders.

2- Agreements on common sets of DNA markers in order to genotype systematically the collections. Using a common set of DNA markers would allow for:

- Accurate measures of genetic diversity within and among global cotton germplasm collections
- Identify redundant genotypes
- Assist in the selection of core sets of germplasm accessions, representing most of the genetic variability, permitting optimization of conservation and of phenotyping.

Germplasm databases incorporating morphological, field performance and molecular data will help to associate specific DNA data with traits of interest.

Linkage of databases worldwide would permit more efficiency: same as with global medical databases, associations unseen with smaller sets of data could be evidenced. Nevertheless, it can be guessed that reluctance and impediments for transfers of data, genetic or phenotypic, should logically be the same as for germplasm exchange.

Interest for all is enormous, and the two tasks could permit to initiate a network between cotton collections worldwide.

Cirad, CRBt

Cirad, in France, develops a great deal of activities around genetic resources, with collections for many crops and other organisms, and research programs for characterization and gene search. The germplasm in CIRAD is managed by the Tropical Biological Resources Centre or CRBt. This structure guaranties a professional management of genetic resources, with specialized researchers and technical staff, including juridical experts. The high quality management includes a total traceability of germplasm, strongly binding European legislation, high international ambitions. Europe aims at registering trusted collections of genetic resources, so scientific and administrative ambitions are high on genetic resources.

For research projects on germplasm resources, Cirad develops partnerships based on a non-monetary system of benefit-sharing, essentially transfers of competences to partner countries, such as high-level technical formations and qualifications, PhD doctorates for to young researchers, and so on.
For research projects on germplasm resources, Cirad develops partnerships based on a non-monetary system of benefit-sharing, essentially transfers of competences to partner countries, such as high-level technical formations and qualifications, PhD doctorates for to young researchers, and so on. The ABS (access and benefit sharing) proposition can also include the management of genetic resources by the CRB-T, in order to secure the traceability of germplasm.
We maintain a cotton collection. It is well characterized with botanical, agronomic and fibre quality descriptors. The cotton collection which was maintained by cotton geneticists is now integrating the Tropical Biological Resources Centre. The cotton collection interacts with institutions worldwide:
- Seed transfers to national agronomic research systems in many countries
- Reconstitution of lost national collections (natural disasters, social events...), on various occasions in recent years
- Research programs in partnership: *e.g.* association genetics for drought resistance genes, genotyping of wild cotton collections
- Backup of cotton genetic improvement programs, bringing diversity.